

Appendix I: BLAST search of GenBank Accession No. W26469 against the human genomic plus transcript (G+T) database

BLASTN 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 301E3H6C01S

Database: Human build 36.3 RNA, reference, and HuRef assemblies

49,942 sequences; 5,818,011,736 total letters

Query= gi|1307375|gb|W26469.1| 32f4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence.

Length=754

Sequences producing significant alignments:	Score (Bits)	E Value
ref NT_007933.14 Hs7_8090 Homo sapiens chromosome 7 genomic c...	426	1e-116
ref NW_001839071.2 Hs7_WGA464_36 Homo sapiens chromosome 7 ge...	426	1e-116
ref NT_024524.13 Hs13_24680 Homo sapiens chromosome 13 genomi...	44.6	0.16
ref NT_019546.15 Hs12_19702 Homo sapiens chromosome 12 genomi...	44.6	0.16
ref NW_001838061.2 Hs12_WGA770_36 Homo sapiens chromosome 12 ...	44.6	0.16
ref NW_001838074.1 Hs13_WGA783_36 Homo sapiens chromosome 13 ...	44.6	0.16
ref NT_033927.7 Hs11_34082 Homo sapiens chromosome 11 genomic...	41.0	2.0
ref NT_008705.15 Hs10_8862 Homo sapiens chromosome 10 genomic...	41.0	2.0
ref NT_009714.16 Hs12_9871 Homo sapiens chromosome 12 genomic...	41.0	2.0
ref NT_008413.17 Hs9_8570 Homo sapiens chromosome 9 genomic c...	41.0	2.0
ref NW_001839149.2 Hs9_WGA542_36 Homo sapiens chromosome 9 ge...	41.0	2.0
ref NW_001837932.2 Hs10_WGA641_36 Homo sapiens chromosome 10 ...	41.0	2.0
ref NW_001838052.1 Hs12_WGA761_36 Homo sapiens chromosome 12 ...	41.0	2.0
ref NW_001838028.2 Hs11_WGA737_36 Homo sapiens chromosome 11 ...	41.0	2.0
ref XM_001715194.1 PREDICTED: Homo sapiens WD repeat domain ...	39.2	6.8
ref XM_293354.9 PREDICTED: Homo sapiens WD repeat domain 42C...	39.2	6.8
ref XM_942624.3 PREDICTED: Homo sapiens WD repeat domain 42C...	39.2	6.8
ref NT_025741.14 Hs6_25897 Homo sapiens chromosome 6 genomic ...	39.2	6.8
ref NT_022517.17 Hs3_22673 Homo sapiens chromosome 3 genomic ...	39.2	6.8
ref NT_026437.11 Hs14_26604 Homo sapiens chromosome 14 genomi...	39.2	6.8
ref NT_006576.15 Hs5_6733 Homo sapiens chromosome 5 genomic c...	39.2	6.8
ref NT_016354.18 Hs4_16510 Homo sapiens chromosome 4 genomic ...	39.2	6.8
ref NT_011757.15 HsX_11914 Homo sapiens chromosome X genomic ...	39.2	6.8
ref NT_022135.15 Hs2_22291 Homo sapiens chromosome 2 genomic ...	39.2	6.8
ref NT_005334.15 Hs2_5491 Homo sapiens chromosome 2 genomic c...	39.2	6.8
ref NT_022184.14 Hs2_22340 Homo sapiens chromosome 2 genomic ...	39.2	6.8
ref NT_010194.16 Hs15_10351 Homo sapiens chromosome 15 genomi...	39.2	6.8
ref NT_023133.12 Hs5_23289 Homo sapiens chromosome 5 genomic ...	39.2	6.8
ref NW_001838218.2 Hs15_WGA927_36 Homo sapiens chromosome 15 ...	39.2	6.8
ref NW_001838848.1 Hs2_WGA241_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838768.1 Hs2_WGA161_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838766.1 Hs2_WGA159_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838920.1 Hs4_WGA313_36 Homo sapiens chromosome 4 ge...	39.2	6.8
ref NW_001838929.1 Hs5_WGA322_36 Homo sapiens chromosome 5 ge...	39.2	6.8
ref NW_001838111.1 Hs14_WGA820_36 Homo sapiens chromosome 14 ...	39.2	6.8
ref NW_001842360.1 HsX_WGA1321_36 Homo sapiens chromosome X g...	39.2	6.8
ref NW_001838954.2 Hs5_WGA347_36 Homo sapiens chromosome 5 ge...	39.2	6.8
ref NW_001838877.2 Hs3_WGA270_36 Homo sapiens chromosome 3 ge...	39.2	6.8

ALIGNMENTS

>ref|NT_007933.14|Hs7_8090 Homo sapiens chromosome 7 genomic contig, reference assem
Length=64426257

Features in this part of subject sequence:
transportin 3

Score = 426 bits (472), Expect = 1e-116
Identities = 250/261 (95%), Gaps = 1/261 (0%)
Strand=Plus/Plus

Query	32	CCTNCATACTTAGTTGTGAGATCCATCCCCTGGCTTCATTCCCTGAACTGGCTTTAGNAA	91
Sbjct	53874301	CCTACATACTTAGTTGTGAGATCCATCCCCTGGCTTCATTCCCTGAACTGGCTTTAG-AA	53874
Query	92	CNCTGGCAGTCTAGCTTATAACCCCCAGGCTGACTAGAGAACTCAAGGTAAAAGCAGCCC	151
Sbjct	53874360	CACTGGCAGTCTAGCTTATAACCCCCAGGCTGACTAGAGAACTCAAGGTAAAAGCAGCCC	53874
Query	152	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGGTTCCCTNCTCGATGA	211
Sbjct	53874420	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGGTTCCCTTCTCGATGA	53874
Query	212	TCCATTAANTGGAAGAGTAACCCAAGAAAACATCATGGANTCCAAGANTCAGTGGATCCA	271
Sbjct	53874480	TCCATTAAATGGAAGAGTAACCCAAGAAAACATCATGGAATCCAAGAATCAGTGGATCCA	53874
Query	272	GCACAANAAGGNGGNAAAGGG	292
Sbjct	53874540	GCACAACAAAGAGGCAAAGGG	53874560

>ref|NW_001839071.2|Hs7_WGA464_36 Homo sapiens chromosome 7 genomic contig, alternat
(based on HuRef SCAF_1103279188381A)
Length=28934855

Features in this part of subject sequence:
transportin 3

Score = 426 bits (472), Expect = 1e-116
Identities = 250/261 (95%), Gaps = 1/261 (0%)
Strand=Plus/Minus

Query	32	CCTNCATACTTAGTTGTGAGATCCATCCCCTGGCTTCATTCCCTGAACTGGCTTTAGNAA	91
Sbjct	2602639	CCTACATACTTAGTTGTGAGATCCATCCCCTGGCTTCATTCCCTGAACTGGCTTTAG-AA	260258
Query	92	CNCTGGCAGTCTAGCTTATAACCCCCAGGCTGACTAGAGAACTCAAGGTAAAAGCAGCCC	151
Sbjct	2602580	CACTGGCAGTCTAGCTTATAACCCCCAGGCTGACTAGAGAACTCAAGGTAAAAGCAGCCC	260252
Query	152	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGGTTCCCTNCTCGATGA	211
Sbjct	2602520	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGGTTCCCTTCTCGATGA	260246
Query	212	TCCATTAANTGGAAGAGTAACCCAAGAAAACATCATGGANTCCAAGANTCAGTGGATCCA	271
Sbjct	2602460	TCCATTAAATGGAAGAGTAACCCAAGAAAACATCATGGAATCCAAGAATCAGTGGATCCA	260240
Query	272	GCACAANAAGGNGGNAAAGGG	292

```

          ||||| || | || |||||
Sbjct  2602400  GCACAACAAAGAGGCAAAGGG  2602380

```

>ref|NT_024524.13|Hs13_24680 Homo sapiens chromosome 13 genomic contig, reference as
Length=67740325

Features flanking this part of subject sequence:

7592 bp at 5' side: hypothetical protein

16093 bp at 3' side: fibronectin type III domain containing 3A isoform 1

Score = 44.6 bits (48), Expect = 0.16

Identities = 32/36 (88%), Gaps = 1/36 (2%)

Strand=Plus/Plus

```

Query  140          TAAAAGCAGCCCAAGAAAAACAGACCAACAGAAAAG  175
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  30544201     TAAAAGCAGCCAAAGAAAAACAGAACAA-AGATAAG  30544235

```

>ref|NT_019546.15|Hs12_19702 Homo sapiens chromosome 12 genomic contig, reference as
Length=32815934

Features flanking this part of subject sequence:

2785 bp at 5' side: D-amino-acid oxidase

9168 bp at 3' side: SV2 related protein

Score = 44.6 bits (48), Expect = 0.16

Identities = 40/48 (83%), Gaps = 2/48 (4%)

Strand=Plus/Plus

```

Query  152          AAGAAA-AACAGACCAACAGAAAAGCAATGAGAGAAAGGAT-GAAGGT  197
          ||||| || ||| || ||||| || ||||| ||||| |||||
Sbjct  32779285     AAGAAAGAAAAGAAGAAAAGAAAAGAAAAGAGAGAAAGGATGGAAGGT  32779332

```

>ref|NW_001838061.2|Hs12_WGA770_36 Homo sapiens chromosome 12 genomic contig, altern
(based on HuRef SCAF_1103279188362)
Length=32873191

Features flanking this part of subject sequence:

8830 bp at 5' side: SV2 related protein

2949 bp at 3' side: D-amino-acid oxidase

Score = 44.6 bits (48), Expect = 0.16

Identities = 40/48 (83%), Gaps = 2/48 (4%)

Strand=Plus/Minus

```

Query  152          AAGAAA-AACAGACCAACAGAAAAGCAATGAGAGAAAGGAT-GAAGGT  197
          ||||| || ||| || ||||| || ||||| ||||| |||||
Sbjct  77998        AAGAAAGAAAAGAAGAAAAGAAAAGAAAAGAGAGAAAGGATGGAAGGT  77951

```

>ref|NW_001838074.1|Hs13_WGA783_36 Homo sapiens chromosome 13 genomic contig, altern
(based on HuRef SCAF_1103279188353)
Length=6801713

Features flanking this part of subject sequence:

7591 bp at 5' side: hypothetical protein

16117 bp at 3' side: fibronectin type III domain containing 3A isoform 1

Score = 44.6 bits (48), Expect = 0.16
Identities = 32/36 (88%), Gaps = 1/36 (2%)
Strand=Plus/Plus

Query	140	TAAAAGCAGCCCAAGAAAAACAGACCAACAGAAAAG	175
Spict	3561241	TAAAAGCAGCCAAAGAAAAACAGAACAA-AGATAAG	3561275

```
>ref|NT_033927.7|Hs11_34082 Homo sapiens chromosome 11 genomic contig, reference assembly
Length=17911127
```

Features in this part of subject sequence:
transmembrane protein 135

Score = 41.0 bits (44), Expect = 2.0
Identities = 27/29 (93%), Gaps = 1/29 (3%)
Strand=Plus/Minus

Query	141	AAAAGCAGCCCAAGAAAAACAGACCAACA	169
Subjct	17085496	AAAAGCAGCCCAAGAAAAA-AGACCCACA	17085469

```
>ref|NT_008705.15|Hs10_8862 Homo sapiens chromosome 10 genomic contig, reference assembly
Length=20794160
```

Features flanking this part of subject sequence:
24944 bp at 5' side: cyclin Y isoform 2
11430 bp at 3' side: connexin40.1

Score = 41.0 bits (44), Expect = 2.0
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Plus

```

Query    154          GAAAAACAGACCAACAGAAAAGCAA    178
          |||||
Sbjct    17858367     GAAAAACAGAACAACAGAAAAGCAA    17858391

```

>ref|NT_009714.16|Hs12_9871 Homo sapiens chromosome 12 genomic contig, reference assembly
Length=27615668

Features flanking this part of subject sequence:
149869 bp at 5' side: intermediate filament tail domain containing 1
352356 bp at 3' side: Ras association (RalGDS/AF-6) domain family 8

Score = 41.0 bits (44), Expect = 2.0
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Plus

Query	140	TAAAAGCAGCCCAAGAAAAACAGAC	164
Sbjct	18614871	TAAAAGCAGCCCAAGAAAAACAGAC	18614895

>ref|NT_008413.17|Hs9_8570 Homo sapiens chromosome 9 genomic contig, reference assembly
Length=39653686

Features flanking this part of subject sequence:

14584 bp at 5' side: FRAS1 related extracellular matrix 1

288432 bp at 3' side: hypothetical protein LOC158219

Score = 41.0 bits (44), Expect = 2.0

Identities = 25/27 (92%), Gaps = 0/27 (0%)

Strand=Plus/Plus

Query	152	AAGAAAAACAGACCAACAGAAAAGCAA	178
Subjct	14873559	AAGAAAAACAGAAACAACAGCAAAGCAA	14873585

>ref|NW_001839149.2|Hs9_WGA542_36 Homo sapiens chromosome 9 genomic contig, alternat
(based on HuRef SCAF 1103279188402)

Length=35741120

Features flanking this part of subject sequence:

288290 bp at 5' side: hypothetical protein LOC158219

14596 bp at 3' side: FRAS1 related extracellular matrix 1

Score = 41.0 bits (44), Expect = 2.0

Identities = 25/27 (92%), Gaps = 0/27 (0%)

Strand=Plus/Minus

Query	152	AAGAAAAACAGACCAACAGAAAAGCAA	178
Subject	21021360	AAGAAAAACAGAAACAACAGCAAAGCAA	21021334

>ref|NW_001837932.2|Hs10_WGA641_36 Homo sapiens chromosome 10 genomic contig, altern
(based on HuRef SCAF 1103279188217B)

Length=7623348

Features flanking this part of subject sequence:

11466 bp at 5' side: connexin40.1

24935 bp at 3' side: cyclin Y isoform 1

Score = 41.0 bits (44), Expect = 2.0

Identities = 24/25 (96%), Gaps = 0/25 (0%)

Strand=Plus/Minus

Query	154	GAAAAACAGACCAACAGAAAAGCAA	178
Sbjct	2804781	GAAAAACAGAACAACAGAAAAGCAA	2804757

>ref|NW_001838052.1|Hs12_WGA761_36 Homo sapiens chromosome 12 genomic contig, altern
(based on HuRef SCAF 1103279188408)

Length=21675488

Features flanking this part of subject sequence:

149615 bp at 5' side: intermediate filament tail domain containing 1

351841 bp at 3' side: Ras association (RalGDS/AF-6) domain family 8

Score = 41.0 bits (44), Expect = 2.0

Identities = 24/25 (96%), Gaps = 0/25 (0%)

Strand=Plus/Plus

Query 140 TAAAAGCAGCCCAAGAAAAACAGAC 164

Sbjct 16266157 TAAAGCAGCCAAAGAAAAACAGAC 16266181

```
>ref|NW_001838028.2|Hs11_WGA737_36 Homo sapiens chromosome 11 genomic contig, altern
(based on HuRef SCAF_1103279187758)
Length=16912879
```

Features in this part of subject sequence:
transmembrane protein 135

Score = 41.0 bits (44), Expect = 2.0
Identities = 27/29 (93%), Gaps = 1/29 (3%)
Strand=Plus/Plus

Query	141	AAAAGCAGCCCAAGAAAAACAGACCAACA	169
Subjct	826512	AAAAGCAGCCCAAGAAAAA-AGACCCACA	826539

>ref|XM_001715194.1| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2979

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

Query	157	AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG	192
Subject	2587	AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG	2552

>ref|XM_293354.9| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2983

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

Query	157	AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG	192
Sbjct	2587	AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG	2552

>ref|XM_942624.3| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2684

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

Query	157	AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG	192
Spict	2587	AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG	2552

```
>ref|NT_025741.14|Hs6_25897 Homo sapiens chromosome 6 genomic contig, reference asse  
Length=61645385
```

Features flanking this part of subject sequence:

65086 bp at 5' side: golgi associated PDZ and coiled-coil motif containing iso...
 8267 bp at 3' side: nuclear undecaprenyl pyrophosphate synthase 1 homolog

Score = 39.2 bits (42), Expect = 6.8
 Identities = 27/31 (87%), Gaps = 0/31 (0%)
 Strand=Plus/Plus

```
Query 166      AACAGAAAAGCAATGAGAGAAAGGATGAAGG 196
              |||||
Sbjct 22157966 AACAGAAAAGCAAAGACAGAAAAGATTAAGG 22157996
```

>ref|NT_022517.17|Hs3_22673 Homo sapiens chromosome 3 genomic contig, reference asse
 Length=66080833

Features flanking this part of subject sequence:
 6402 bp at 5' side: SREBF chaperone protein
 46654 bp at 3' side: transmembrane protein 103

Score = 39.2 bits (42), Expect = 6.8
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```
Query 170      GAAAAGCAATGAGAGAAAGGA 190
              |||||
Sbjct 47430889 GAAAAGCAATGAGAGAAAGGA 47430909
```

>ref|NT_026437.11|Hs14_26604 Homo sapiens chromosome 14 genomic contig, reference as
 Length=88290585

Features in this part of subject sequence:
 pellino 2

Score = 39.2 bits (42), Expect = 6.8
 Identities = 24/27 (88%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

```
Query 266      GATCCAGCACAAANAAGGNGGNAAGGG 292
              |||||
Sbjct 37708443 GATCCAGCACAGAAGGCGGCAAAGGG 37708469
```

>ref|NT_006576.15|Hs5_6733 Homo sapiens chromosome 5 genomic contig, reference assem
 Length=46378398

Features flanking this part of subject sequence:
 1398867 bp at 5' side: cadherin 12, type 2 preproprotein
 31459 bp at 3' side: PR domain containing 9

Score = 39.2 bits (42), Expect = 6.8
 Identities = 31/35 (88%), Gaps = 2/35 (5%)
 Strand=Plus/Plus

```
Query 152      AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAA 186
              |||||
Sbjct 23450409 AAGAAAAATAGACCAACAGAACAG-AAT-AGAGAA 23450441
```

>ref|NT_016354.18|Hs4_16510 Homo sapiens chromosome 4 genomic contig, reference asse

Length=92123751

Features flanking this part of subject sequence:

1597372 bp at 5' side: FAT tumor suppressor homolog 4

532822 bp at 3' side: hypothetical protein

Score = 39.2 bits (42), Expect = 6.8

Identities = 24/26 (92%), Gaps = 0/26 (0%)

Strand=Plus/Plus

```

Query    152      AAGAAAAACAGACCAACAGAAAAGCA    177
          |||||
Sbjct    52558442 AAGAAAAACAAACCAACAGAAAATCA    52558467

```

```
>ref|NT_011757.15|HsX_11914 Homo sapiens chromosome X genomic contig, reference asse  
Length=34879939
```

Features flanking this part of subject sequence:

182 bp at 5' side: similar to hCG19378

72299 bp at 3' side: melanoma antigen family B, 10

Score = 39.2 bits (42), Expect = 6.8

Identities = 30/36 (83%), Gaps = 0/36 (0%)

Strand=Plus/Minus

Query	157	AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG	192
Sbjct	25548808	AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG	25548773

>ref|NT_022135.15|Hs2_22291 Homo sapiens chromosome 2 genomic contig, reference assemblage
Length=38390280

Features in this part of subject sequence:

contactin associated protein-like 5

Score = 39.2 bits (42), Expect = 6.8

Identities = 36/46 (78%), Gaps = 0/46 (0%)

Strand=Plus/Plus

Query	151	CAAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGG		196
Sbjct	13818771	CAACAAAAACAGACCAAAAAAAAAAAAAAAAAAGATGAAGG		13818816

```
>ref|NT_005334.15|Hs2_5491 Homo sapiens chromosome 2 genomic contig, reference assem
Length=11088087
```

Features flanking this part of subject sequence:

189392 bp at 5' side: hypothetical protein LOC348738

19739 bp at 3' side: hippocalcin-like 1

Score = 39.2 bits (42), Expect = 6.8

Identities = 27/31 (87%), Gaps = 0/31 (0%)

Strand=Plus/Plus

Query	165	CAACAGAAAAAGCAATGAGAGAAAGGATGAAG	195
Subject	5374250	CAACAAAACAGAAATGAGAGAAAGGATCAAG	5374280

>ref|NT_022184.14|Hs2_22340 Homo sapiens chromosome 2 genomic contig, reference assemblage
Length=68373980

Features in this part of subject sequence:
ATPase family, AAA domain containing 2B

Score = 39.2 bits (42), Expect = 6.8
Identities = 26/29 (89%), Gaps = 0/29 (0%)
Strand=Plus/Plus

```
Query 157      AACAGACCAACAGAAAAGCAATGAGAGA 185
              |||
Sbjct 2952937 AACAGACCAACAGAAAAGAACAGAGAGA 2952965
```

>ref|NT_010194.16|Hs15_10351 Homo sapiens chromosome 15 genomic contig, reference assemblage
Length=53619965

Features in this part of subject sequence:
RAR-related orphan receptor A isoform b
RAR-related orphan receptor A isoform c

Score = 39.2 bits (42), Expect = 6.8
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

```
Query 158      AACAGACCAACAGAAAAGCAA 178
              |||
Sbjct 31676505 AACAGACCAACAGAAAAGCAA 31676485
```

>ref|NT_023133.12|Hs5_23289 Homo sapiens chromosome 5 genomic contig, reference assemblage
Length=25714846

Features in this part of subject sequence:
RAN binding protein 17

Score = 39.2 bits (42), Expect = 6.8
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

```
Query 142      AAAGCAGCCCAAGAAAAACAG 162
              |||
Sbjct 15287688 AAAGCAGCCCAAGAAAAACAG 15287668
```

>ref|NW_001838218.2|Hs15_WGA927_36 Homo sapiens chromosome 15 genomic contig, alternate (based on HuRef SCAF_1103279188258)
Length=30371087

Features in this part of subject sequence:
RAR-related orphan receptor A isoform c
RAR-related orphan receptor A isoform b

Score = 39.2 bits (42), Expect = 6.8
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```

Query   158          AACAGACCAACAGAAAAGCAA   178
          |||||
Sbjct   13482804    AACAGACCAACAGAAAAGCAA   13482824

```

>ref|NW_001838848.1|Hs2_WGA241_36 Homo sapiens chromosome 2 genomic contig, alternat
(based on HuRef SCAF_1103279188208)
Length=5768927

Features in this part of subject sequence:
contactin associated protein-like 5

Score = 39.2 bits (42), Expect = 6.8
Identities = 36/46 (78%), Gaps = 0/46 (0%)
Strand=Plus/Plus

```

Query   151          CAAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGG   196
          ||| |||||
Sbjct   3959290    CAACAAAAACAGACCAAAAAAAAAAAAAAAAAAAAAAGATGAAGG   3959335

```

>ref|NW_001838768.1|Hs2_WGA161_36 Homo sapiens chromosome 2 genomic contig, alternat
(based on HuRef SCAF_1103279188306)
Length=8993619

Features in this part of subject sequence:
ATPase family, AAA domain containing 2B

Score = 39.2 bits (42), Expect = 6.8
Identities = 26/29 (89%), Gaps = 0/29 (0%)
Strand=Plus/Plus

```

Query   157          AAACAGACCAACAGAAAAGCAATGAGAGA   185
          |||||
Sbjct   2966183    AAACAGACCAACAGAAAAGAACAGAGAGA   2966211

```

>ref|NW_001838766.1|Hs2_WGA159_36 Homo sapiens chromosome 2 genomic contig, alternat
(based on HuRef SCAF_1103279187422)
Length=8347242

Features flanking this part of subject sequence:
190464 bp at 5' side: hypothetical protein LOC348738
19733 bp at 3' side: hippocalcin-like 1

Score = 39.2 bits (42), Expect = 6.8
Identities = 27/31 (87%), Gaps = 0/31 (0%)
Strand=Plus/Plus

```

Query   165          CAACAGAAAAGCAATGAGAGAAAGGATGAAG   195
          |||| || || ||
Sbjct   2637447    CAACAAAACAGAAATGAGAGAAAGGATCAAG   2637477

```

>ref|NW_001838920.1|Hs4_WGA313_36 Homo sapiens chromosome 4 genomic contig, alternat
(based on HuRef SCAF_1103279188303)
Length=20364230

Features flanking this part of subject sequence:
1597064 bp at 5' side: FAT tumor suppressor homolog 4

532542 bp at 3' side: hypothetical protein

Score = 39.2 bits (42), Expect = 6.8
Identities = 24/26 (92%), Gaps = 0/26 (0%)
Strand=Plus/Plus

Query	152	AAGAAAAACAGACCAACAGAAAAGCA	177
Sbjct	8584868	AAGAAAAACAAACCAACAGAAAATCA	8584893

```
>ref|NW_001838929.1|Hs5_WGA322_36 Homo sapiens chromosome 5 genomic contig, alternat
(based on HuRef SCAF_1103279188406C)
Length=12799137
```

Features flanking this part of subject sequence:
 1399583 bp at 5' side: cadherin 12, type 2 preproprotein
 31453 bp at 3' side: PR domain containing 9

Score = 39.2 bits (42), Expect = 6.8
Identities = 31/35 (88%), Gaps = 2/35 (5%)
Strand=Plus/Plus

Query	152	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAA	186
Sbjct	2083999	AAGAAAAATAGACCAACAGAACAG-AAT-AGAGAA	2084031

```
>ref|NW_001838111.1|Hs14_WGA820_36 Homo sapiens chromosome 14 genomic contig, altern
(based on HuRef SCAF_1103279187954)
Length=25156336
```

Features in this part of subject sequence:
pellino 2

Score = 39.2 bits (42), Expect = 6.8
Identities = 24/27 (88%), Gaps = 0/27 (0%)
Strand=Plus/Plus

Query	266	GATCCAGCACAAANAAGGNGGNAAAGGG	292
Sbjct	15574420	GATCCAGCACAAAGAAGGCGGCAAAGGG	15574446

```
>ref|NW_001842360.1|HsX_WGA1321_36 Homo sapiens chromosome X genomic contig, alterna
(based on HuRef SCAF_1103279188416)
Length=28681338
```

Features flanking this part of subject sequence:
182 bp at 5' side: hypothetical protein
72349 bp at 3' side: melanoma antigen family B, 10

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

Query	157	AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG	192
Subject	19297887	AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG	19297852

>ref|NW_001838954.2|Hs5_WGA347_36 Homo sapiens chromosome 5 genomic contig, alternat
(based on HuRef SCAF_1103279188298)
Length=20179980

Features in this part of subject sequence:
RAN binding protein 17

Score = 39.2 bits (42), Expect = 6.8
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query  142      AAAGCAGCCCAAGAAAAACAG  162
          |||
Sbjct  4886351  AAAGCAGCCCAAGAAAAACAG  4886371
```

>ref|NW_001838877.2|Hs3_WGA270_36 Homo sapiens chromosome 3 genomic contig, alternat
(based on HuRef SCAF_1103279188143)
Length=55925128

Features flanking this part of subject sequence:
46504 bp at 5' side: transmembrane protein 103
6392 bp at 3' side: SREBF chaperone protein

Score = 39.2 bits (42), Expect = 6.8
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus

```
Query  170      GAAAAGCAATGAGAGAAAGGA  190
          |||
Sbjct  18731141  GAAAAGCAATGAGAGAAAGGA  18731121
```

Database: Human build 36.3 RNA, reference, and HuRef assemblies
Posted date: Dec 2, 2008 11:49 AM
Number of letters in database: 1,523,044,440
Number of sequences in database: 49,942

```
Lambda      K      H
    0.634    0.408    0.912
```

Gapped

```
Lambda      K      H
    0.625    0.410    0.780
```

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 49942

Number of Hits to DB: 1626165

Number of extensions: 83827

Number of successful extensions: 160

Number of sequences better than 10: 4

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 160

Number of HSP's successfully gapped: 4

Length of query: 754

Length of database: 5818011736

Length adjustment: 34

Effective length of query: 720

Effective length of database: 5816313708

Effective search space: 4187745869760
Effective search space used: 4187745869760
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 34 (31.9 bits)
S2: 42 (39.2 bits)